

10/593425

H 06291/PCT

SEQUENCE LISTING

<110> Henkel Kommanditgesellschaft auf Aktien

<120> Der Faktor RecA aus Bacillus licheniformis und recA-inaktivierte Sicherheitsstämme für die biotechnologische Produktion

<130> H 06291 PCT

<150> DE102004013988

<151> 2004-03-19

<160> 32

<170> PatentIn version 3.1

<210> 1

<211> 1047

<212> DNA

<213> Bacillus licheniformis DSM 13

<220>

<221> CDS

<222> (1)..(1047)

<223>

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<222> (1)..(1047)

<223> recA

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aag cag ttt ggt aaa ggt tcg att atg aaa ctc ggc gaa caa act gaa	96
Lys Gln Phe Gly Lys Gly Ser Ile Met Lys Leu Gly Glu Gln Thr Glu	
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acg aga att tca aca gtt ccg agc ggt tct tta gcg ctc gat gcg gct	144
Thr Arg Ile Ser Thr Val Pro Ser Gly Ser Leu Ala Leu Asp Ala Ala	
35 40 45	
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Leu Gly Val Gly Gly Tyr Pro Arg Gly Arg Ile Ile Glu Val Tyr Gly	
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cct gaa agc tcc ggt aaa acg acg gtg gcg ctt cat gcg att gcc gaa	240
Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu	
65 70 75 80	
gtt cag cag cag ggc gga caa gcg gcg ttc atc gac gcc gac acc gcg	288
Val Gln Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Asp Thr Ala	
85 90 95	
ctt gat ccc gtc tat gca caa aag ctg ggc gtc aac att gat gag ctt	336
Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp Glu Leu	
100 105 110	

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Ser	Gly	Ala	Ile	Asn	Lys	Ser	Lys	Thr	Ile	Ala	Ile	Phe	Ile	Asn	Gln	
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Gly	Gly	Arg	Ala	Leu	Lys	Phe	Tyr	Ser	Ser	Val	Arg	Leu	Glu	Val	Arg	
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Arg	Ala	Glu	Gln	Leu	Lys	Gln	Gly	Asn	Asp	Val	Met	Gly	Asn	Lys	Thr	
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Tyr	Ser	Tyr	Gln	Glu	Glu	Arg	Leu	Gly	Gln	Gly	Arg	Glu	Asn	Ala	Lys	
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Gln	Phe	Leu	Lys	Glu	Asn	Lys	Asp	Ile	Leu	Leu	Met	Ile	Gln	Glu	Gln	
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<210> 2
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 <212> PRT
 <213> Bacillus licheniformis DSM 13

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 35 40 45

Leu Gly Val Gly Gly Tyr Pro Arg Gly Arg Ile Ile Glu Val Tyr Gly
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Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu
 65 70 75 80

Val Gln Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Asp Thr Ala
 85 90 95

Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp Glu Leu
 100 105 110

Leu Leu Ser Gln Pro Asp Thr Gly Glu Gln Ala Leu Glu Ile Ala Glu
 115 120 125

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 130 135 140

Ala Ala Leu Val Pro Lys Ala Glu Ile Glu Gly Asp Met Gly Asp Ser
 145 150 155 160

His Val Gly Leu Gln Ala Arg Leu Met Ser Gln Ala Leu Arg Lys Leu
 165 170 175

Ser Gly Ala Ile Asn Lys Ser Lys Thr Ile Ala Ile Phe Ile Asn Gln
 180 185 190

Ile Arg Glu Lys Val Gly Val Met Phe Gly Asn Pro Glu Thr Thr Pro
 195 200 205

Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Val Arg Leu Glu Val Arg

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210	215	220
Arg Ala Glu Gln Leu Lys Gln Gly Asn Asp Val Met Gly Asn Lys Thr		
225	230	235 240
Lys Ile Lys Val Val Lys Asn Lys Val Ala Pro Pro Phe Arg Thr Ala		
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Glu Val Asp Ile Met Tyr Gly Glu Gly Ile Ser Lys Glu Gly Glu Ile		
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Ile Asp Leu Gly Thr Glu Leu Asp Ile Val Gln Lys Ser Gly Ala Trp		
	275	280 285
Tyr Ser Tyr Gln Glu Glu Arg Leu Gly Gln Gly Arg Glu Asn Ala Lys		
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Gln Phe Leu Lys Glu Asn Lys Asp Ile Leu Leu Met Ile Gln Glu Gln		
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<210> 3
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 <212> DNA
 <213> Bacillus licheniformis

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 <223> spoIV

<220>
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 <222> (140)..(142)
 <223> First codon translated as Met.

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aagtcggggg gaaagaagc gtg aag aat aaa tgg ctt tct ttt ttt tca gga 172
          Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly
          1          5          10

aag atc cag ctt aag ata acg gga aaa ggg atc gaa cgg tta tta aat 220
Lys Ile Gln Leu Lys Ile Thr Gly Lys Gly Ile Glu Arg Leu Leu Asn
          15          20          25

gaa tgc acc agg cgc aac atc ccg atg ttt aat gta aag aaa aag aaa 268
Glu Cys Thr Arg Arg Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys
          30          35          40

gac gcc gtc ttt ctt tat att ccg ctt tct gat gta cat gcc ttc cgg 316
Asp Ala Val Phe Leu Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg
          45          50          55

aag gtc atc aga ggc ttc gac tgc aag tgc agg ttc atc aaa cga aaa 364
Lys Val Ile Arg Gly Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys
60          65          70          75

ggg ttt cct ttc ctc gtg cag aag tct aaa cgg aat agc ggc ttc act 412
Gly Phe Pro Phe Leu Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr
          80          85          90

ttt gga gtt gct gca ttt ttt atc atc atg ctc cta ttg tcc aac atg 460
Phe Gly Val Ala Ala Phe Phe Ile Ile Met Leu Leu Leu Ser Asn Met
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ctt tgg aaa att gat att aca gga gcc aat ccg gag aca gaa cat caa 508
Leu Trp Lys Ile Asp Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln
          110          115          120

atc aaa cag caa ttg gat caa atc ggc gtc aaa aaa ggc cgc ttt cag 556
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          125          130          135

ttt tca atg ctg acc ccg gaa aaa att cag cag gcg ctc aca aag cgg 604
Phe Ser Met Leu Thr Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg
140          145          150          155

gtc gaa aac atc act tgg gtg ggt att gag tta aac ggc acc gcc ctt 652
Val Glu Asn Ile Thr Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu
          160          165          170

cac atg aaa gtc gtt gaa aag aat gaa cct gac aaa gaa aaa tat atc 700
His Met Lys Val Val Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile
          175          180          185

ggt ccg agg cac atc gtc gcc aaa aaa ggg gcg acc atc tcg aaa aag 748
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          190          195          200

ttc gtg gaa aaa ggc gag ccg ctc gtc acg gtg aac cag cac gtt gaa 796
Phe Val Glu Lys Gly Glu Pro Leu Val Thr Val Asn Gln His Val Glu
          205          210          215

aaa ggg caa atg ctc gtt tcc ggg ctg atc gga agc gaa gag gaa aag 844
Lys Gly Gln Met Leu Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys
220          225          230          235

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Ser Thr Val Thr Val Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly	
255 260 265	
aaa gta agg aca agt cac aag cta tcc ctc gga tca ttt tcc gtg ccg	988
Lys Val Arg Thr Ser His Lys Leu Ser Leu Gly Ser Phe Ser Val Pro	
270 275 280	
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285 290 295	
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Glu Thr Glu Asn Pro Ser Leu His Phe Met Asn Phe Lys Leu Pro Val	
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Ala Tyr Glu Lys Glu His Met Arg Glu Ser Glu Gln Ile Lys Arg Val	
320 325 330	
tac tcg aaa aaa gaa gca gtt ctt gaa gga atc gaa atg gga aaa aga	1180
Tyr Ser Lys Lys Glu Ala Val Leu Glu Gly Ile Glu Met Gly Lys Arg	
335 340 345	
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Asp Ile Arg Lys Lys Ile Gly Ser Asp Gly Asn Ile Ile Ser Glu Lys	
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Val Leu His Glu Thr Ser Glu Asn Gly Lys Val Lys Leu Ile Ile Leu	
365 370 375	
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Tyr Gln Val Ile Glu Asp Ile Val Gln Thr Thr Pro Ile Val Gln Glu	
380 385 390 395	
act aaa gaa tga cagaacactt acttgcaatt catcagcaac tggaaagtcc	1376
Thr Lys Glu	
gaatgaggct caaacgctgt ttgggaacca ggattcccat ttgaagttga tggaggaaga	1436
gctgaacatt tcaattgtca cgcgcgagaga aaccgtgtat gtgacaggag atgaagaaac	1496
gtttgaaatc gcggacagcc tgcttgccctc tctcctaaat ctgatccgca aaggaatcga	1556
gatatccgaa cgcgatgtct tgtatgcgat caagatggcg aaaaagcaga agcttgagtt	1616
ttttgaaagc atgtatgaag aggaaattac gaaaaacgcc aaaggaaaac cgatcagagt	1676
caaaaccatc ggtcaaagag aatacatcgc cgccatgaaa aggcacgact taatcttcgg	1736
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<211> 398

<212> PRT

<213> Bacillus licheniformis

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<221> misc_feature

<222> (140)..(142)

<223> First codon translated as Met.

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20 25 30

Asn Ile Pro Met Phe Asn Val Lys Lys Lys Lys Asp Ala Val Phe Leu
35 40 45

Tyr Ile Pro Leu Ser Asp Val His Ala Phe Arg Lys Val Ile Arg Gly
50 55 60

Phe Asp Cys Lys Cys Arg Phe Ile Lys Arg Lys Gly Phe Pro Phe Leu
65 70 75 80

Val Gln Lys Ser Lys Arg Asn Ser Gly Phe Thr Phe Gly Val Ala Ala
85 90 95

Phe Phe Ile Ile Met Leu Leu Leu Ser Asn Met Leu Trp Lys Ile Asp
100 105 110

Ile Thr Gly Ala Asn Pro Glu Thr Glu His Gln Ile Lys Gln Gln Leu
115 120 125

Asp Gln Ile Gly Val Lys Lys Gly Arg Phe Gln Phe Ser Met Leu Thr
130 135 140

Pro Glu Lys Ile Gln Gln Ala Leu Thr Lys Arg Val Glu Asn Ile Thr
145 150 155 160

Trp Val Gly Ile Glu Leu Asn Gly Thr Ala Leu His Met Lys Val Val
165 170 175

Glu Lys Asn Glu Pro Asp Lys Glu Lys Tyr Ile Gly Pro Arg His Ile
180 185 190

Val Ala Lys Lys Gly Ala Thr Ile Ser Lys Lys Phe Val Glu Lys Gly
195 200 205

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Glu Pro Leu Val Thr Val Asn Gln His Val Glu Lys Gly Gln Met Leu
210 215 220

Val Ser Gly Leu Ile Gly Ser Glu Glu Glu Lys Gln Lys Val Gly Ala
225 230 235 240

Lys Gly Lys Ile Tyr Gly Glu Thr Trp Tyr Lys Ser Thr Val Thr Val
245 250 255

Pro Leu Glu Thr Ser Phe Asp Val Phe Thr Gly Lys Val Arg Thr Ser
260 265 270

His Lys Leu Ser Leu Gly Ser Phe Ser Val Pro Ile Trp Gly Phe Ser
275 280 285

Phe Lys Lys Glu Asp Phe Ser Arg Pro Lys Thr Glu Thr Glu Asn Pro
290 295 300

Ser Leu His Phe Met Asn Phe Lys Leu Pro Val Ala Tyr Glu Lys Glu
305 310 315 320

His Met Arg Glu Ser Glu Gln Ile Lys Arg Val Tyr Ser Lys Lys Glu
325 330 335

Ala Val Leu Glu Gly Ile Glu Met Gly Lys Arg Asp Ile Arg Lys Lys
340 345 350

Ile Gly Ser Asp Gly Asn Ile Ile Ser Glu Lys Val Leu His Glu Thr
355 360 365

Ser Glu Asn Gly Lys Val Lys Leu Ile Ile Leu Tyr Gln Val Ile Glu
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<212> DNA
<213> Bacillus subtilis

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 ttcttccgga agagatactt ttggagggta cgattgatgt cgttcgatat gttgagtcacat 180
 aaagccgagg gggaaatggt gtg aaa aat aaa tgg ctg tct ttt ttt tcg ggt 233
 Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly
 1 5 10
 aag gtc cag ctt gaa ttg acg gga aga ggg att gag cgg ctc ctt aat 281
 Lys Val Gln Leu Glu Leu Thr Gly Arg Gly Ile Glu Arg Leu Leu Asn
 15 20 25
 gaa tgc aca aaa cag ggg att ccg gtc ttt cat gtc aaa aaa aag aaa 329
 Glu Cys Thr Lys Gln Gly Ile Pro Val Phe His Val Lys Lys Lys Lys
 30 35 40
 gaa gcc gta tcg tta tat ata cag ctt cag gat gta cat gcc ttt cgg 377
 Glu Ala Val Ser Leu Tyr Ile Gln Leu Gln Asp Val His Ala Phe Arg
 45 50 55
 cgg gta aga agt aaa ttt aaa tgt aaa gcc cga ttt atc aat cgg aag 425
 Arg Val Arg Ser Lys Phe Lys Cys Lys Ala Arg Phe Ile Asn Arg Lys
 60 65 70 75
 gga ttt ccc ttc ctg ttg ctg aaa tca aag ctg aat ata ggg ttt acg 473
 Gly Phe Pro Phe Leu Leu Lys Ser Lys Leu Asn Ile Gly Phe Thr
 80 85 90
 atc ggt ttt gcg att ttt ttc att ctt ttg ttt ttg ctg tcc aat atg 521
 Ile Gly Phe Ala Ile Phe Phe Ile Leu Leu Phe Leu Leu Ser Asn Met
 95 100 105
 gtg tgg aaa att gat gtg aca ggc gct aag cct gaa aca gaa cat caa 569
 Val Trp Lys Ile Asp Val Thr Gly Ala Lys Pro Glu Thr Glu His Gln
 110 115 120
 atg agg cag cat ctt aat gaa atc ggc gtc aaa aag ggc cgt ctg cag 617
 Met Arg Gln His Leu Asn Glu Ile Gly Val Lys Lys Gly Arg Leu Gln
 125 130 135
 ttt tta atg atg tcg ccc gaa aaa ata cag aaa tca tta acc aat gga 665
 Phe Leu Met Met Ser Pro Glu Lys Ile Gln Lys Ser Leu Thr Asn Gly
 140 145 150 155
 ata gac aat atc act tgg gtc gga gtt gat ctg aag ggg acg acc att 713
 Ile Asp Asn Ile Thr Trp Val Gly Val Asp Leu Lys Gly Thr Thr Ile

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175								180				185					
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Ser	Pro	Arg	Asn	Ile	Val	Ala	Lys	Lys	Lys	Ala	Thr	Ile	Thr	Arg	Met		
190								195				200					
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205								210				215					
aag	gga	cag	ctg	ctt	gtt	tcg	gga	ctg	atc	ggc	agc	gaa	gac	cat	cag	905	
Lys	Gly	Gln	Leu	Leu	Val	Ser	Gly	Leu	Ile	Gly	Ser	Glu	Asp	His	Gln		
220								225				230				235	
cag	gaa	gtc	gcc	tca	aaa	gca	gaa	att	tat	gga	gaa	acc	tg	tat	aga	953	
Gln	Glu	Val	Ala	Ser	Lys	Ala	Glu	Ile	Tyr	Gly	Glu	Thr	Trp	Tyr	Arg		
240								245				250					
tca	gaa	gtg	aca	gtc	ccg	ctt	gaa	aca	tta	ttt	aac	gtc	tat	acg	ggc	1001	
Ser	Glu	Val	Thr	Val	Pro	Leu	Glu	Thr	Leu	Phe	Asn	Val	Tyr	Thr	Gly		
255								260				265					
aaa	gta	agg	aca	aag	cac	aag	ctt	tct	ttt	ggt	tct	ttg	gca	atc	ccg	1049	
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285								290				295					
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Ser	Tyr	Val	Lys	Glu	Gln	Thr	Arg	Glu	Ser	Glu	Glu	Ala	Leu	Arg	Lys		
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335								340				345					
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Asp	Val	Glu	Asp	Lys	Ile	Gly	Glu	Asn	Gly	Glu	Val	Lys	Ser	Glu	Lys		
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Val	Leu	His	Gln	Thr	Val	Glu	Asn	Gly	Lys	Val	Lys	Leu	Ile	Ile	Leu		
365								370				375					
tac	caa	gtt	ata	gaa	gat	atc	gtt	caa	acc	aca	cct	att	gtc	agg	gag	1385	
Tyr	Gln	Val	Ile	Glu	Asp	Ile	Val	Gln	Thr	Thr	Pro	Ile	Val	Arg	Glu		
380								385				390				395	
act	gaa	gaa	tga	cagaacattt	acttgcgatg	aatcaaaaac	tgaaaaaccc									1437	
Thr	Glu	Glu															

H 06291/PCT

ggacgaggcg ctttcactct tcgggaacca agattctttt ttgaaattga tggagaaaga 1497
tctgaattta aatatcatta cgcgcggcga gacgatttat gtttcaggcg atgatgaatc 1557
gtttcagatt gcagacaggc tgctgggata gctcctc 1594

<210> 6
<211> 398
<212> PRT
<213> Bacillus subtilis

<220>
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<222> (201)..(203)
<223> First codon translated as Met.

<400> 6

Val Lys Asn Lys Trp Leu Ser Phe Phe Ser Gly Lys Val Gln Leu Glu
1 5 10 15

Leu Thr Gly Arg Gly Ile Glu Arg Leu Leu Asn Glu Cys Thr Lys Gln
20 25 30

Gly Ile Pro Val Phe His Val Lys Lys Lys Lys Glu Ala Val Ser Leu
35 40 45

Tyr Ile Gln Leu Gln Asp Val His Ala Phe Arg Arg Val Arg Ser Lys
50 55 60

Phe Lys Cys Lys Ala Arg Phe Ile Asn Arg Lys Gly Phe Pro Phe Leu
65 70 75 80

Leu Leu Lys Ser Lys Leu Asn Ile Gly Phe Thr Ile Gly Phe Ala Ile
85 90 95

Phe Phe Ile Leu Leu Phe Leu Leu Ser Asn Met Val Trp Lys Ile Asp
100 105 110

Val Thr Gly Ala Lys Pro Glu Thr Glu His Gln Met Arg Gln His Leu
115 120 125

Asn Glu Ile Gly Val Lys Lys Gly Arg Leu Gln Phe Leu Met Met Ser
130 135 140

Pro Glu Lys Ile Gln Lys Ser Leu Thr Asn Gly Ile Asp Asn Ile Thr
145 150 155 160

Trp Val Gly Val Asp Leu Lys Gly Thr Thr Ile His Met Lys Val Val

			165						170						175		
Glu	Lys	Asn	Glu	Pro	Glu	Lys	Glu	Lys	Tyr	Val	Ser	Pro	Arg	Asn	Ile		
			180							185				190			
Val	Ala	Lys	Lys	Lys	Ala	Thr	Ile	Thr	Arg	Met	Ser	Val	Gln	Lys	Gly		
			195							200				205			
Gln	Pro	Met	Ala	Ala	Ile	His	Asp	His	Val	Glu	Lys	Gly	Gln	Leu	Leu		
			210				215							220			
Val	Ser	Gly	Leu	Ile	Gly	Ser	Glu	Asp	His	Gln	Gln	Glu	Val	Ala	Ser		
225							230				235						
Lys	Ala	Glu	Ile	Tyr	Gly	Glu	Thr	Trp	Tyr	Arg	Ser	Glu	Val	Thr	Val		
						245				250							
Pro	Leu	Glu	Thr	Leu	Phe	Asn	Val	Tyr	Thr	Gly	Lys	Val	Arg	Thr	Lys		
						260				265				270			
His	Lys	Leu	Ser	Phe	Gly	Ser	Leu	Ala	Ile	Pro	Ile	Trp	Gly	Met	Thr		
						275				280				285			
Phe	Lys	Lys	Glu	Glu	Leu	Lys	His	Pro	Lys	Thr	Glu	Gln	Glu	Lys	His		
						290							300				
Ser	Leu	His	Phe	Leu	Gly	Phe	Lys	Leu	Pro	Val	Ser	Tyr	Val	Lys	Glu		
305							310				315						
Gln	Thr	Arg	Glu	Ser	Glu	Glu	Ala	Leu	Arg	Lys	Tyr	Thr	Lys	Glu	Glu		
						325				330							
Ala	Val	Gln	Glu	Gly	Ile	Lys	Leu	Gly	Lys	Gln	Asp	Val	Glu	Asp	Lys		
						340				345				350			
Ile	Gly	Glu	Asn	Gly	Glu	Val	Lys	Ser	Glu	Lys	Val	Leu	His	Gln	Thr		
						355				360				365			
Val	Glu	Asn	Gly	Lys	Val	Lys	Leu	Ile	Ile	Leu	Tyr	Gln	Val	Ile	Glu		
						370							380				
Asp	Ile	Val	Gln	Thr	Thr	Pro	Ile	Val	Arg	Glu	Thr	Glu	Glu				
385							390				395						

77

H 06291/PCT

<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (201)..(1679)
<223>

<220>
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<222> (201)..(203)
<223> First codon translated as Met.

<220>
<221> gene
<222> (1)..(1876)
<223> spoIVA

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atgatatgaa aaaggaatga acctttctcc cttgcataca aatagggaga aagggtttttt 60
tatattaata gattgaggat gagaaatttt ctaaagatgt catattcaaa taggacaacg 120
tcatacacat atagtgtcct gtgtttgatt gaaagagctt aataaaaattg aaaaggatag 180
gaagtcgagg aggggatcac ttg gaa aag gtc gat att ttc aag gat atc gct 233
Leu Glu Lys Val Asp Ile Phe Lys Asp Ile Ala
1 5 10
gaa cga aca gga ggc gat ata tac tta gga gtc gta ggt gct gtc cgt 281
Glu Arg Thr Gly Gly Asp Ile Tyr Leu Gly Val Val Gly Ala Val Arg
15 20 25
aca gga aaa tcc acg ttc att aaa aaa ttt atg gag ctt gtg gtg ctc 329
Thr Gly Lys Ser Thr Phe Ile Lys Lys Phe Met Glu Leu Val Val Leu
30 35 40
ccg aat atc agt aac gaa gca gac cgg gcc cga gcg cag gat gaa ctg 377
Pro Asn Ile Ser Asn Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu
45 50 55
ccg cag agc gca gcc ggc aaa acc att atg act aca gag cct aaa ttt 425
Pro Gln Ser Ala Ala Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe
60 65 70 75
gtt ccg aat cag gcg atg tct gtt cat gtg tca gac gga ctc gat gtg 473
Val Pro Asn Gln Ala Met Ser Val His Val Ser Asp Gly Leu Asp Val
80 85 90
aat ata aga tta gta gat tgt gta ggt tac aca gtg ccc ggc gct aaa 521
Asn Ile Arg Leu Val Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys
95 100 105
gga tat gaa gat gaa aac ggg ccg cgg atg atc aat acg cct tgg tac 569
Gly Tyr Glu Asp Glu Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr
110 115 120
gaa gaa ccg atc cca ttt cat gag gct gct gaa atc ggc aca cga aaa 617

H 06291/PCT

Glu	Glu	Pro	Ile	Pro	Phe	His	Glu	Ala	Ala	Glu	Ile	Gly	Thr	Arg	Lys		
125						130					135						
gtc	att	caa	gaa	cac	tcg	acc	atc	gga	gtt	gtc	att	acg	aca	gac	ggc	665	
Val	Ile	Gln	Glu	His	Ser	Thr	Ile	Gly	Val	Val	Ile	Thr	Thr	Asp	Gly	155	
140					145					150							
acc	att	gga	gat	atc	gcc	aga	agt	gac	tat	ata	gag	gct	gaa	gaa	aga	713	
Thr	Ile	Gly	Asp	Ile	Ala	Arg	Ser	Asp	Tyr	Ile	Glu	Ala	Glu	Glu	Arg	170	
				160					165								
gtc	att	gaa	gag	ctg	aaa	gag	gtt	ggc	aaa	cct	ttt	att	atg	gtc	atc	761	
Val	Ile	Glu	Glu	Leu	Lys	Glu	Val	Gly	Lys	Pro	Phe	Ile	Met	Val	Ile	185	
			175					180									
aac	tca	gtc	agg	ccg	tat	cac	ccg	gaa	acg	gaa	gcc	atg	cgc	cag	gat	809	
Asn	Ser	Val	Arg	Pro	Tyr	His	Pro	Glu	Thr	Glu	Ala	Met	Arg	Gln	Asp	200	
		190					195										
tta	agc	gaa	aaa	tat	gat	atc	ccg	gta	ttg	gca	atg	agt	gta	gag	agc	857	
Leu	Ser	Glu	Lys	Tyr	Asp	Ile	Pro	Val	Leu	Ala	Met	Ser	Val	Glu	Ser	215	
	205					210											
atg	cgg	gaa	tca	gat	gtg	ctg	agt	gtg	ctc	aga	gag	gcc	ctc	tac	gag	905	
Met	Arg	Glu	Ser	Asp	Val	Leu	Ser	Val	Leu	Arg	Glu	Ala	Leu	Tyr	Glu	235	
	220				225					230							
ttt	ccg	gtg	cta	gaa	gtg	aat	gtc	aat	ctc	cca	agc	tgg	gta	atg	gtg	953	
Phe	Pro	Val	Leu	Glu	Val	Asn	Val	Asn	Leu	Pro	Ser	Trp	Val	Met	Val	250	
				240					245								
ctg	aaa	gaa	aac	cat	tgg	ttg	cgt	gaa	agc	tat	cag	gag	tcc	gtg	aag	1001	
Leu	Lys	Glu	Asn	His	Trp	Leu	Arg	Glu	Ser	Tyr	Gln	Glu	Ser	Val	Lys	265	
			255					260									
gaa	acg	gtt	aag	gat	att	aaa	cgg	ctc	cgg	gac	gta	gac	agg	gtt	gtc	1049	
Glu	Thr	Val	Lys	Asp	Ile	Lys	Arg	Leu	Arg	Asp	Val	Asp	Arg	Val	Val	280	
		270					275										
ggc	caa	ttc	agc	gag	ttt	gaa	ttc	att	gaa	agt	gcc	gga	tta	gcc	gga	1097	
Gly	Gln	Phe	Ser	Glu	Phe	Glu	Phe	Ile	Glu	Ser	Ala	Gly	Leu	Ala	Gly	295	
	285					290											
att	gag	ctg	ggc	caa	ggg	gtg	gca	gaa	att	gat	ttg	tac	gcg	cct	gat	1145	
Ile	Glu	Leu	Gly	Gln	Gly	Val	Ala	Glu	Ile	Asp	Leu	Tyr	Ala	Pro	Asp	315	
	300				305					310							
cat	cta	tat	gat	caa	atc	cta	aaa	gaa	gtt	gtg	ggc	gtc	gaa	atc	aga	1193	
His	Leu	Tyr	Asp	Gln	Ile	Leu	Lys	Glu	Val	Val	Gly	Val	Glu	Ile	Arg	330	
				320					325								
gga	aga	gac	cat	ctg	ctt	gag	ctc	atg	caa	gac	ttc	gcc	cat	gcg	aaa	1241	
Gly	Arg	Asp	His	Leu	Leu	Glu	Leu	Met	Gln	Asp	Phe	Ala	His	Ala	Lys	345	
			335					340									
aca	gaa	tat	gat	caa	gtg	tct	gat	gcc	tta	aaa	atg	gtc	aaa	cag	acg	1289	
Thr	Glu	Tyr	Asp	Gln	Val	Ser	Asp	Ala	Leu	Lys	Met	Val	Lys	Gln	Thr	360	
		350					355										
gga	tac	ggc	att	gca	gcg	cct	gct	tta	gct	gat	atg	agt	ctc	gat	gag	1337	
Gly	Tyr	Gly	Ile	Ala	Ala	Pro	Ala	Leu	Ala	Asp	Met	Ser	Leu	Asp	Glu		

H 06291/PCT

365	370	375	
ccg gaa att ata agg cag ggc tcg cga ttc ggt gtg agg ctg aaa gct			1385
Pro Glu Ile Ile Arg Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala			
380	385	390	395
gtc gct ccg tcg atc cat atg atc aaa gta gat gtc gaa agc gaa ttc			1433
Val Ala Pro Ser Ile His Met Ile Lys Val Asp Val Glu Ser Glu Phe			
	400	405	410
gcc ccg att atc gga acg gaa aaa caa agt gaa gag ctt gta cgc tat			1481
Ala Pro Ile Ile Gly Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr			
	415	420	425
tta atg cag gac ttt gag gat gat ccg ctc tcc atc tgg aat tcc gat			1529
Leu Met Gln Asp Phe Glu Asp Asp Pro Leu Ser Ile Trp Asn Ser Asp			
	430	435	440
atc ttc gga agg tcg ctg agc tca att gtg aga gaa ggg att cag gca			1577
Ile Phe Gly Arg Ser Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala			
	445	450	455
aag ctg tca ttg atg cct gaa aac gca cgg tat aaa tta aaa gaa aca			1625
Lys Leu Ser Leu Met Pro Glu Asn Ala Arg Tyr Lys Leu Lys Glu Thr			
	460	465	470
tta gaa aga atc ata aac gaa ggc tct ggc ggc tta atc gcc atc atc			1673
Leu Glu Arg Ile Ile Asn Glu Gly Ser Gly Gly Leu Ile Ala Ile Ile			
	480	485	490
ctg taa taccggtaga cctctttata gaatgggagg tcttttttct ttgctcttaa			1729
Leu			
taatggaaaa ggatcaagga ataggatgaa aaaaggaaaa aaaggaatat tcgttcggta			1789
aatcacctta aatccttgac gagcaaggga ttgacgcttt aaaatgcttg atatggcttt			1849
ttatatgtgt tactctacat acagaaa			1876

<210> 8
 <211> 492
 <212> PRT
 <213> Bacillus subtilis

<220>
 <221> misc_feature
 <222> (201)..(203)
 <223> First codon translated as Met.

<400> 8

Leu	Glu	Lys	Val	Asp	Ile	Phe	Lys	Asp	Ile	Ala	Glu	Arg	Thr	Gly	Gly
1				5					10					15	

Asp	Ile	Tyr	Leu	Gly	Val	Val	Gly	Ala	Val	Arg	Thr	Gly	Lys	Ser	Thr
			20					25					30		

H 06291/PCT

Phe Ile Lys Lys Phe Met Glu Leu Val Val Leu Pro Asn Ile Ser Asn
 35 40 45

 Glu Ala Asp Arg Ala Arg Ala Gln Asp Glu Leu Pro Gln Ser Ala Ala
 50 55 60

 Gly Lys Thr Ile Met Thr Thr Glu Pro Lys Phe Val Pro Asn Gln Ala
 65 70 75 80

 Met Ser Val His Val Ser Asp Gly Leu Asp Val Asn Ile Arg Leu Val
 85 90 95

 Asp Cys Val Gly Tyr Thr Val Pro Gly Ala Lys Gly Tyr Glu Asp Glu
 100 105 110

 Asn Gly Pro Arg Met Ile Asn Thr Pro Trp Tyr Glu Glu Pro Ile Pro
 115 120 125

 Phe His Glu Ala Ala Glu Ile Gly Thr Arg Lys Val Ile Gln Glu His
 130 135 140

 Ser Thr Ile Gly Val Val Ile Thr Thr Asp Gly Thr Ile Gly Asp Ile
 145 150 155 160

 Ala Arg Ser Asp Tyr Ile Glu Ala Glu Glu Arg Val Ile Glu Glu Leu
 165 170 175

 Lys Glu Val Gly Lys Pro Phe Ile Met Val Ile Asn Ser Val Arg Pro
 180 185 190

 Tyr His Pro Glu Thr Glu Ala Met Arg Gln Asp Leu Ser Glu Lys Tyr
 195 200 205

 Asp Ile Pro Val Leu Ala Met Ser Val Glu Ser Met Arg Glu Ser Asp
 210 215 220

 Val Leu Ser Val Leu Arg Glu Ala Leu Tyr Glu Phe Pro Val Leu Glu
 225 230 235 240

 Val Asn Val Asn Leu Pro Ser Trp Val Met Val Leu Lys Glu Asn His
 245 250 255

 Trp Leu Arg Glu Ser Tyr Gln Glu Ser Val Lys Glu Thr Val Lys Asp
 260 265 270

 Ile Lys Arg Leu Arg Asp Val Asp Arg Val Val Gly Gln Phe Ser Glu

H 06291/PCT

275	280	285
Phe Glu Phe Ile Glu Ser Ala Gly Leu Ala Gly Ile Glu Leu Gly Gln		
290	295	300
Gly Val Ala Glu Ile Asp Leu Tyr Ala Pro Asp His Leu Tyr Asp Gln		
305	310	315
Ile Leu Lys Glu Val Val Gly Val Glu Ile Arg Gly Arg Asp His Leu		
325	330	335
Leu Glu Leu Met Gln Asp Phe Ala His Ala Lys Thr Glu Tyr Asp Gln		
340	345	350
Val Ser Asp Ala Leu Lys Met Val Lys Gln Thr Gly Tyr Gly Ile Ala		
355	360	365
Ala Pro Ala Leu Ala Asp Met Ser Leu Asp Glu Pro Glu Ile Ile Arg		
370	375	380
Gln Gly Ser Arg Phe Gly Val Arg Leu Lys Ala Val Ala Pro Ser Ile		
385	390	395
His Met Ile Lys Val Asp Val Glu Ser Glu Phe Ala Pro Ile Ile Gly		
405	410	415
Thr Glu Lys Gln Ser Glu Glu Leu Val Arg Tyr Leu Met Gln Asp Phe		
420	425	430
Glu Asp Asp Pro Leu Ser Ile Trp Asn Ser Asp Ile Phe Gly Arg Ser		
435	440	445
Leu Ser Ser Ile Val Arg Glu Gly Ile Gln Ala Lys Leu Ser Leu Met		
450	455	460
Pro Glu Asn Ala Arg Tyr Lys Leu Lys Glu Thr Leu Glu Arg Ile Ile		
465	470	475
Asn Glu Gly Ser Gly Gly Leu Ile Ala Ile Ile Leu		
485	490	

<210> 9
 <211> 1675
 <212> DNA
 <213> Bacillus subtilis
 <220>

H 06291/PCT

<221> CDS
<222> (201)..(1478)
<223>

<220>
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<222> (1)..(1675)
<223> spoIVB

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acatccattc gttcatcagt atatccaatg tttttcttca tatgacagtt ataaataagc 120
cgtcagaagg caaaattaaa tgatgtagca gcaagtcata aagaagggtgt gggataggag 180
cgaggagagt gaagtagtga atg ccc gat aac atc aga aaa gca gta ggt tta 233
      Met Pro Asp Asn Ile Arg Lys Ala Val Gly Leu
      1             5             10
att ctc ctt gtt tcg tta tta agt gta ggt tta tgc aaa ccg cta aaa 281
Ile Leu Leu Val Ser Leu Leu Ser Val Gly Leu Cys Lys Pro Leu Lys
      15             20             25
gaa tat tta ctg att cca acg caa atg aga gta ttt gaa acc caa aca 329
Glu Tyr Leu Leu Ile Pro Thr Gln Met Arg Val Phe Glu Thr Gln Thr
      30             35             40
caa gcg att gaa acg agt tta tcg gta aat gct cag aca tca gaa tcc 377
Gln Ala Ile Glu Thr Ser Leu Ser Val Asn Ala Gln Thr Ser Glu Ser
      45             50             55
tca gaa gcg ttt aca gta aag aaa gat ccg cat gaa atc aag gtg acg 425
Ser Glu Ala Phe Thr Val Lys Lys Asp Pro His Glu Ile Lys Val Thr
      60             65             70             75
ggc aaa aaa tca ggt gag tca gaa ttg gta tat gat ctt gcc gga ttt 473
Gly Lys Lys Ser Gly Glu Ser Glu Leu Val Tyr Asp Leu Ala Gly Phe
      80             85             90
cca att aaa aaa aca aaa gtg cat gtt ctt cct gat tta aaa gtt ata 521
Pro Ile Lys Lys Thr Lys Val His Val Leu Pro Asp Leu Lys Val Ile
      95             100             105
cct ggc gga caa tca atc ggt gta aaa ctt cat tcc gtc ggt gtt ctt 569
Pro Gly Gly Gln Ser Ile Gly Val Lys Leu His Ser Val Gly Val Leu
      110             115             120
gtc gga ttt cat caa atc aat aca agt gaa ggc aaa aaa tct ccg gga 617
Val Gly Phe His Gln Ile Asn Thr Ser Glu Gly Lys Lys Ser Pro Gly
      125             130             135
gaa acg gca gga att gaa gcg ggc gac atc att att gag atg aat gga 665
Glu Thr Ala Gly Ile Glu Ala Gly Asp Ile Ile Ile Glu Met Asn Gly
      140             145             150             155
cag aaa att gaa aaa atg aat gat gta gcc cca ttt att caa aag gct 713
Gln Lys Ile Glu Lys Met Asn Asp Val Ala Pro Phe Ile Gln Lys Ala
      160             165             170

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H 06291/PCT

ggg	aaa	act	ggt	gaa	tct	tta	gac	tta	ctg	atc	aaa	cgt	gat	aaa	cag	761
Gly	Lys	Thr	Gly	Glu	Ser	Leu	Asp	Leu	Leu	Ile	Lys	Arg	Asp	Lys	Gln	
			175					180					185			
aaa	atc	aaa	acg	aag	ctg	atc	cca	gaa	aag	gat	gaa	gga	gaa	ggc	aaa	809
Lys	Ile	Lys	Thr	Lys	Leu	Ile	Pro	Glu	Lys	Asp	Glu	Gly	Glu	Gly	Lys	
		190					195					200				
tac	aga	atc	ggg	tta	tat	atc	aga	gat	tct	gct	gct	ggc	atc	ggc	act	857
Tyr	Arg	Ile	Gly	Leu	Tyr	Ile	Arg	Asp	Ser	Ala	Ala	Gly	Ile	Gly	Thr	
	205					210					215					
atg	acc	ttt	tat	gaa	ccg	aaa	aca	aaa	aaa	tac	gga	gca	ctt	ggc	cac	905
Met	Thr	Phe	Tyr	Glu	Pro	Lys	Thr	Lys	Lys	Tyr	Gly	Ala	Leu	Gly	His	
220					225					230					235	
gtg	att	tcc	gat	atg	gac	aca	aag	aaa	cca	att	gta	gtg	gag	aat	gga	953
Val	Ile	Ser	Asp	Met	Asp	Thr	Lys	Lys	Pro	Ile	Val	Val	Glu	Asn	Gly	
				240					245					250		
gaa	atc	gtt	aaa	tcc	act	gta	aca	tca	att	gaa	aaa	ggg	aca	ggc	ggt	1001
Glu	Ile	Val	Lys	Ser	Thr	Val	Thr	Ser	Ile	Glu	Lys	Gly	Thr	Gly	Gly	
			255					260					265			
aat	ccg	gga	gaa	aaa	ctg	gcg	cga	ttt	tcc	tca	gaa	cgc	aaa	acg	atc	1049
Asn	Pro	Gly	Glu	Lys	Leu	Ala	Arg	Phe	Ser	Ser	Glu	Arg	Lys	Thr	Ile	
		270					275					280				
ggg	gat	att	aac	aga	aac	agc	ccg	ttt	ggg	att	ttc	ggc	aca	ctg	cat	1097
Gly	Asp	Ile	Asn	Arg	Asn	Ser	Pro	Phe	Gly	Ile	Phe	Gly	Thr	Leu	His	
	285					290					295					
cag	ccg	att	caa	aac	aac	ata	tca	gat	caa	gca	ttg	ccg	gtt	gcg	ttt	1145
Gln	Pro	Ile	Gln	Asn	Asn	Ile	Ser	Asp	Gln	Ala	Leu	Pro	Val	Ala	Phe	
300					305					310					315	
tct	acc	gaa	gtc	aaa	aaa	ggg	ccg	gct	gaa	att	tta	acg	gtt	att	gat	1193
Ser	Thr	Glu	Val	Lys	Lys	Gly	Pro	Ala	Glu	Ile	Leu	Thr	Val	Ile	Asp	
				320					325					330		
gat	gac	aaa	gta	gaa	aaa	ttc	gat	att	gaa	atc	gtc	agc	aca	acg	ccg	1241
Asp	Asp	Lys	Val	Glu	Lys	Phe	Asp	Ile	Glu	Ile	Val	Ser	Thr	Thr	Pro	
			335					340					345			
caa	aaa	ttc	cct	gcg	aca	aaa	gga	atg	gtg	ttg	aaa	att	acc	gat	cca	1289
Gln	Lys	Phe	Pro	Ala	Thr	Lys	Gly	Met	Val	Leu	Lys	Ile	Thr	Asp	Pro	
		350					355					360				
aga	ctg	ttg	aaa	gaa	aca	gga	ggc	atc	gta	cag	ggg	atg	agc	gga	agc	1337
Arg	Leu	Leu	Lys	Glu	Thr	Gly	Gly	Ile	Val	Gln	Gly	Met	Ser	Gly	Ser	
	365					370					375					
ccg	atc	att	caa	aat	gga	aaa	gtg	atc	ggt	gct	gtc	acc	cat	gta	ttt	1385
Pro	Ile	Ile	Gln	Asn	Gly	Lys	Val	Ile	Gly	Ala	Val	Thr	His	Val	Phe	
380					385					390					395	
gta	aat	gac	ccg	aca	agc	ggc	tac	ggt	gtt	cat	att	gaa	tgg	atg	ctg	1433
Val	Asn	Asp	Pro	Thr	Ser	Gly	Tyr	Gly	Val	His	Ile	Glu	Trp	Met	Leu	
				400					405					410		

H 06291/PCT

tca gaa gca gga atc gat att tat gga aaa gaa aaa gca agc tga 1478
 Ser Glu Ala Gly Ile Asp Ile Tyr Gly Lys Glu Lys Ala Ser
 415 420 425

ctgccggagt ttccggcagt ttttttattt tgatccctct tcacttctca gaatacatac 1538
 ggtaaaatat acaaaagaag atttttcgac aaattcacgt ttccttggtt gtcaaatttc 1598
 attttttagtc gaaaaacaga gaaaaacata gaataacaaa gatatgccac taatattggt 1658
 gattatgatt ttttttag 1675

<210> 10
 <211> 425
 <212> PRT
 <213> Bacillus subtilis

<400> 10

Met Pro Asp Asn Ile Arg Lys Ala Val Gly Leu Ile Leu Leu Val Ser
 1 5 10 15

Leu Leu Ser Val Gly Leu Cys Lys Pro Leu Lys Glu Tyr Leu Leu Ile
 20 25 30

Pro Thr Gln Met Arg Val Phe Glu Thr Gln Thr Gln Ala Ile Glu Thr
 35 40 45

Ser Leu Ser Val Asn Ala Gln Thr Ser Glu Ser Ser Glu Ala Phe Thr
 50 55 60

Val Lys Lys Asp Pro His Glu Ile Lys Val Thr Gly Lys Lys Ser Gly
 65 70 75 80

Glu Ser Glu Leu Val Tyr Asp Leu Ala Gly Phe Pro Ile Lys Lys Thr
 85 90 95

Lys Val His Val Leu Pro Asp Leu Lys Val Ile Pro Gly Gly Gln Ser
 100 105 110

Ile Gly Val Lys Leu His Ser Val Gly Val Leu Val Gly Phe His Gln
 115 120 125

Ile Asn Thr Ser Glu Gly Lys Lys Ser Pro Gly Glu Thr Ala Gly Ile
 130 135 140

Glu Ala Gly Asp Ile Ile Ile Glu Met Asn Gly Gln Lys Ile Glu Lys
 145 150 155 160

Met Asn Asp Val Ala Pro Phe Ile Gln Lys Ala Gly Lys Thr Gly Glu

175

Ser Gly Tyr Gly Val His Ile Glu Trp Met Leu Ser Glu Ala Gly Ile
405 410 415

H 06291/PCT

Asp Ile Tyr Gly Lys Glu Lys Ala Ser
420 425

<210> 11
<211> 1900
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (201)..(1703)
<223>

<220>
<221> gene
<222> (1)..(1900)
<223> spoIVCA

<220>
<221> misc_feature
<222> (201)..(203)
<223> First codon translated as Met.

<400> 11
ttttgcatat tcattgaaac gtttaataac actatagttt aattttaaact ctcctcattt 60
ggacaaacag ctgttacata gcattaccca aggggtgatg cattttatga aagtgataat 120
catcgaggga cgcgaagctg acaaatgcat taacgattgc tatcattatt taataaaact 180
ttataggaag gagattcagg gtg ata gca ata tat gta agg gta tcg acc gag 233
Val Ile Ala Ile Tyr Val Arg Val Ser Thr Glu
1 5 10
gaa caa gcg atc aag gga tcg agc atc gac agc caa atc gag gcc tgt 281
Glu Gln Ala Ile Lys Gly Ser Ser Ile Asp Ser Gln Ile Glu Ala Cys
15 20 25
ata aag aaa gca ggg act aaa gat gtg ctg aag tat gca gat gaa gga 329
Ile Lys Lys Ala Gly Thr Lys Asp Val Leu Lys Tyr Ala Asp Glu Gly
30 35 40
ttt tca gga gag ctt tta gaa cgt ccg gct ttg aat cgc ttg agg gag 377
Phe Ser Gly Glu Leu Leu Glu Arg Pro Ala Leu Asn Arg Leu Arg Glu
45 50 55
gat gca agc aag gga ctt ata agt caa gtc att tgt tac gat cct gac 425
Asp Ala Ser Lys Gly Leu Ile Ser Gln Val Ile Cys Tyr Asp Pro Asp
60 65 70 75
cgt ctt tct cgg aaa tta atg aat cag cta atc att gat gac gaa ttg 473
Arg Leu Ser Arg Lys Leu Met Asn Gln Leu Ile Ile Asp Asp Glu Leu
80 85 90
cga aag cga aac ata cct ttg att ttt gta aat ggt gaa tac gcc aat 521

H 06291/PCT

Arg	Lys	Arg	Asn	Ile	Pro	Leu	Ile	Phe	Val	Asn	Gly	Glu	Tyr	Ala	Asn		
			95					100					105				
tct	cca	gaa	ggg	caa	ttg	ttt	ttc	gca	atg	cgc	ggg	gca	atc	tca	gaa		569
Ser	Pro		Gly	Gln	Leu	Phe	Phe	Ala	Met	Arg	Gly	Ala	Ile	Ser	Glu		
		110					115					120					
ttt	gaa	aaa	gcc	aaa	atc	aaa	gaa	cgg	aca	tca	agc	ggc	cga	ctt	caa		617
Phe	Glu	Lys	Ala	Lys	Ile	Lys	Glu	Arg	Thr	Ser	Ser	Gly	Arg	Leu	Gln		
	125					130					135						
aaa	atg	aaa	aaa	ggc	atg	atc	att	aaa	gat	tct	aaa	cta	tat	ggc	tat		665
Lys	Met	Lys	Lys	Gly	Met	Ile	Ile	Lys	Asp	Ser	Lys	Leu	Tyr	Gly	Tyr		
140					145					150					155		
aaa	ttt	gtt	aaa	gag	aaa	aga	act	ctt	gag	ata	tta	gaa	gag	gaa	gca		713
Lys	Phe	Val	Lys	Glu	Lys	Arg	Thr	Leu	Glu	Ile	Leu	Glu	Glu	Glu	Ala		
				160					165						170		
aaa	atc	att	cgg	atg	att	ttt	aac	tat	ttc	acc	gat	cat	aaa	agc	cct		761
Lys	Ile	Ile	Arg	Met	Ile	Phe	Asn	Tyr	Phe	Thr	Asp	His	Lys	Ser	Pro		
			175					180					185				
ttt	ttc	ggc	aga	gta	aat	ggg	att	gct	cta	cat	tta	act	cag	atg	ggg		809
Phe	Phe	Gly	Arg	Val	Asn	Gly	Ile	Ala	Leu	His	Leu	Thr	Gln	Met	Gly		
		190				195						200					
gtt	aaa	aca	aaa	aaa	ggc	gcc	aaa	gta	tgg	cac	agg	cag	gtt	gtt	cgg		857
Val	Lys	Thr	Lys	Lys	Gly	Ala	Lys	Val	Trp	His	Arg	Gln	Val	Val	Arg		
	205					210					215						
caa	ata	tta	atg	aac	tct	tcc	tat	aag	ggg	gaa	cat	aga	cag	tat	aaa		905
Gln	Ile	Leu	Met	Asn	Ser	Ser	Tyr	Lys	Gly	Glu	His	Arg	Gln	Tyr	Lys		
220					225					230					235		
tat	gat	aca	gag	ggg	tcc	tat	gtt	tca	aag	cag	gca	ggg	aac	aaa	tct		953
Tyr	Asp	Thr	Glu	Gly	Ser	Tyr	Val	Ser	Lys	Gln	Ala	Gly	Asn	Lys	Ser		
				240					245					250			
ata	att	aaa	ata	agg	cct	gaa	gaa	gaa	caa	atc	act	gtg	aca	att	cca		1001
Ile	Ile	Lys	Ile	Arg	Pro	Glu	Glu	Glu	Gln	Ile	Thr	Val	Thr	Ile	Pro		
			255					260					265				
gca	att	gtt	cca	gct	gaa	caa	tgg	gat	tat	gct	caa	gaa	ctc	tta	ggg		1049
Ala	Ile	Val	Pro	Ala	Glu	Gln	Trp	Asp	Tyr	Ala	Gln	Glu	Leu	Leu	Gly		
		270					275					280					
caa	agt	aaa	aga	aaa	cac	ttg	agt	atc	agc	cct	cac	aat	tac	ttg	tta		1097
Gln	Ser	Lys	Arg	Lys	His	Leu	Ser	Ile	Ser	Pro	His	Asn	Tyr	Leu	Leu		
	285					290					295						
tcg	ggg	ttg	gtt	aga	tgc	gga	aaa	tgc	gga	aat	acc	atg	aca	ggg	aag		1145
Ser	Gly	Leu	Val	Arg	Cys	Gly	Lys	Cys	Gly	Asn	Thr	Met	Thr	Gly	Lys		
300					305					310					315		
aaa	aga	aaa	tca	cat	ggg	aaa	gac	tac	tat	gta	tat	act	tgc	cgg	aaa		1193
Lys	Arg	Lys	Ser	His	Gly	Lys	Asp	Tyr	Tyr	Val	Tyr	Thr	Cys	Arg	Lys		
				320					325					330			
aat	tat	tct	ggc	gca	aag	gac	cgc	ggc	tgc	gga	aaa	gaa	atg	tct	gag		1241
Asn	Tyr	Ser	Gly	Ala	Lys	Asp	Arg	Gly	Cys	Gly	Lys	Glu	Met	Ser	Glu		

H 06291/PCT

	335	340	345	
aat aaa ttg aac cgg cat gta tgg ggt gaa att ttt aaa ttc atc aca				1289
Asn Lys Leu Asn Arg His Val Trp Gly Glu Ile Phe Lys Phe Ile Thr	350	355	360	
aat cct caa aag tat gtt tct ttt aaa gag gct gaa caa tca aat cac				1337
Asn Pro Gln Lys Tyr Val Ser Phe Lys Glu Ala Glu Gln Ser Asn His	365	370	375	
ctg tct gat gaa tta gaa ctt att gaa aaa gag ata gag aaa aca aaa				1385
Leu Ser Asp Glu Leu Glu Leu Ile Glu Lys Glu Ile Glu Lys Thr Lys	380	385	390	395
aaa ggc cgc aag cgt ctt tta acg cta atc agc cta agc gat gac gat				1433
Lys Gly Arg Lys Arg Leu Leu Thr Leu Ile Ser Leu Ser Asp Asp Asp	400	405	410	
gat tta gac ata gat gaa atc aaa gca caa att att gaa ctg caa aaa				1481
Asp Leu Asp Ile Asp Glu Ile Lys Ala Gln Ile Ile Glu Leu Gln Lys	415	420	425	
aag caa aat cag ctt act gaa aag tgt aac aga atc cag tca aaa atg				1529
Lys Gln Asn Gln Leu Thr Glu Lys Cys Asn Arg Ile Gln Ser Lys Met	430	435	440	
aaa gtc cta gat gat acg agc tca agt gaa aat gct cta aaa aga gcc				1577
Lys Val Leu Asp Asp Thr Ser Ser Ser Glu Asn Ala Leu Lys Arg Ala	445	450	455	
atc gac tat ttt caa tca atc ggt gca gat aac tta act ctt gaa gat				1625
Ile Asp Tyr Phe Gln Ser Ile Gly Ala Asp Asn Leu Thr Leu Glu Asp	460	465	470	475
aaa aaa aca att gtt aac ttt atc gtg aaa gaa gtt acc att gtg gat				1673
Lys Lys Thr Ile Val Asn Phe Ile Val Lys Glu Val Thr Ile Val Asp	480	485	490	
tct gac acc ata tat att gaa acg tat taa agaggggtgt atgcaccccc				1723
Ser Asp Thr Ile Tyr Ile Glu Thr Tyr	495	500		
cttttgtaat tacaatctca ttttcaatac acctcgctgc atacgtcgcc acctttgtcc				1783
cttttccagc ggaatagctt tcaattcctt taataagccc gatcgttccg atggagatta				1843
agtcctctgc atcctcacct gtatttttgcga acttttttcac aatatgggcg accaagc				1900

<210> 12
 <211> 500
 <212> PRT
 <213> Bacillus subtilis

<220>
 <221> misc_feature
 <222> (201)..(203)
 <223> First codon translated as Met.

<400> 12

H 06291/PCT

Val Ile Ala Ile Tyr Val Arg Val Ser Thr Glu Glu Gln Ala Ile Lys
1 5 10 15

Gly Ser Ser Ile Asp Ser Gln Ile Glu Ala Cys Ile Lys Lys Ala Gly
20 25 30

Thr Lys Asp Val Leu Lys Tyr Ala Asp Glu Gly Phe Ser Gly Glu Leu
35 40 45

Leu Glu Arg Pro Ala Leu Asn Arg Leu Arg Glu Asp Ala Ser Lys Gly
50 55 60

Leu Ile Ser Gln Val Ile Cys Tyr Asp Pro Asp Arg Leu Ser Arg Lys
65 70 75 80

Leu Met Asn Gln Leu Ile Ile Asp Asp Glu Leu Arg Lys Arg Asn Ile
85 90 95

Pro Leu Ile Phe Val Asn Gly Glu Tyr Ala Asn Ser Pro Glu Gly Gln
100 105 110

Leu Phe Phe Ala Met Arg Gly Ala Ile Ser Glu Phe Glu Lys Ala Lys
115 120 125

Ile Lys Glu Arg Thr Ser Ser Gly Arg Leu Gln Lys Met Lys Lys Gly
130 135 140

Met Ile Ile Lys Asp Ser Lys Leu Tyr Gly Tyr Lys Phe Val Lys Glu
145 150 155 160

Lys Arg Thr Leu Glu Ile Leu Glu Glu Glu Ala Lys Ile Ile Arg Met
165 170 175

Ile Phe Asn Tyr Phe Thr Asp His Lys Ser Pro Phe Phe Gly Arg Val
180 185 190

Asn Gly Ile Ala Leu His Leu Thr Gln Met Gly Val Lys Thr Lys Lys
195 200 205

Gly Ala Lys Val Trp His Arg Gln Val Val Arg Gln Ile Leu Met Asn
210 215 220

Ser Ser Tyr Lys Gly Glu His Arg Gln Tyr Lys Tyr Asp Thr Glu Gly
225 230 235 240

Ser Tyr Val Ser Lys Gln Ala Gly Asn Lys Ser Ile Ile Lys Ile Arg

H 06291/PCT

245										250					255				
Pro	Glu	Glu	Glu	Gln	Ile	Thr	Val	Thr	Ile	Pro	Ala	Ile	Val	Pro	Ala				
			260					265					270						
Glu	Gln	Trp	Asp	Tyr	Ala	Gln	Glu	Leu	Leu	Gly	Gln	Ser	Lys	Arg	Lys				
		275					280					285							
His	Leu	Ser	Ile	Ser	Pro	His	Asn	Tyr	Leu	Leu	Ser	Gly	Leu	Val	Arg				
	290					295					300								
Cys	Gly	Lys	Cys	Gly	Asn	Thr	Met	Thr	Gly	Lys	Lys	Arg	Lys	Ser	His				
305					310					315					320				
Gly	Lys	Asp	Tyr	Tyr	Val	Tyr	Thr	Cys	Arg	Lys	Asn	Tyr	Ser	Gly	Ala				
				325					330					335					
Lys	Asp	Arg	Gly	Cys	Gly	Lys	Glu	Met	Ser	Glu	Asn	Lys	Leu	Asn	Arg				
			340					345					350						
His	Val	Trp	Gly	Glu	Ile	Phe	Lys	Phe	Ile	Thr	Asn	Pro	Gln	Lys	Tyr				
		355					360					365							
Val	Ser	Phe	Lys	Glu	Ala	Glu	Gln	Ser	Asn	His	Leu	Ser	Asp	Glu	Leu				
	370					375					380								
Glu	Leu	Ile	Glu	Lys	Glu	Ile	Glu	Lys	Thr	Lys	Lys	Gly	Arg	Lys	Arg				
385					390					395					400				
Leu	Leu	Thr	Leu	Ile	Ser	Leu	Ser	Asp	Asp	Asp	Asp	Leu	Asp	Ile	Asp				
				405					410					415					
Glu	Ile	Lys	Ala	Gln	Ile	Ile	Glu	Leu	Gln	Lys	Lys	Gln	Asn	Gln	Leu				
			420					425					430						
Thr	Glu	Lys	Cys	Asn	Arg	Ile	Gln	Ser	Lys	Met	Lys	Val	Leu	Asp	Asp				
		435					440					445							
Thr	Ser	Ser	Ser	Glu	Asn	Ala	Leu	Lys	Arg	Ala	Ile	Asp	Tyr	Phe	Gln				
	450					455					460								
Ser	Ile	Gly	Ala	Asp	Asn	Leu	Thr	Leu	Glu	Asp	Lys	Lys	Thr	Ile	Val				
465					470					475					480				
Asn	Phe	Ile	Val	Lys	Glu	Val	Thr	Ile	Val	Asp	Ser	Asp	Thr	Ile	Tyr				
				485					490					495					

H 06291/PCT

Ile Glu Thr Tyr
500

<210> 13
<211> 868
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (201)..(671)
<223>

<220>
<221> gene
<222> (1)..(868)
<223> spoIVCB

<400> 13
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tttttaacat ttgaagtttag tatgctgctt accaaagccg gactcccccg cgagaaattt 120
cccggtagac acacagacag cctccccggtc acatacattt acatataggc ttttgcctac 180
atacttttgt ggaggtgacg atg gtg aca ggt gtt ttc gca gcg ctc ggc ttt 233
Met Val Thr Gly Val Phe Ala Ala Leu Gly Phe
1 5 10
gtt gtt aaa gag ctt gtc ttt tta gta tct tac gtg aaa aac aat gcc 281
Val Val Lys Glu Leu Val Phe Leu Val Ser Tyr Val Lys Asn Asn Ala
15 20 25
ttt cca caa ccg ctc tca agc agc gaa gaa aaa aaa tac tta gag ctc 329
Phe Pro Gln Pro Leu Ser Ser Ser Glu Glu Lys Lys Tyr Leu Glu Leu
30 35 40
atg gct aaa ggg gat gaa cat gcc aga aac atg ctg att gag cat aat 377
Met Ala Lys Gly Asp Glu His Ala Arg Asn Met Leu Ile Glu His Asn
45 50 55
ctt cgc ttg gtc gcc cat att gtg aaa aag ttc gaa aat aca ggt gag 425
Leu Arg Leu Val Ala His Ile Val Lys Lys Phe Glu Asn Thr Gly Glu
60 65 70 75
gat gca gag gac tta atc tcc atc gga acg atc ggg ctt att aaa gga 473
Asp Ala Glu Asp Leu Ile Ser Ile Gly Thr Ile Gly Leu Ile Lys Gly
80 85 90
att gaa agc tat tcc gct gga aaa ggg aca aag gtg gcg acg tat gca 521
Ile Glu Ser Tyr Ser Ala Gly Lys Gly Thr Lys Val Ala Thr Tyr Ala
95 100 105
gcg agg tgt att gaa aat gag att gta att aca aaa ggg ggg tgc ata 569
Ala Arg Cys Ile Glu Asn Glu Ile Val Ile Thr Lys Gly Gly Cys Ile
110 115 120

H 06291/PCT

cac ccc tct tta ata cgt ttc aat ata tat ggt gtc aga atc cac aat 617
His Pro Ser Leu Ile Arg Phe Asn Ile Tyr Gly Val Arg Ile His Asn
125 130 135

ggt aac ttc ttt cac gat aaa gtt aac aat tgt ttt ttt atc ttc aag 665
Gly Asn Phe Phe His Asp Lys Val Asn Asn Cys Phe Phe Ile Phe Lys
140 145 150 155

agt taa gttatctgca ccgattgatt gaaaatagtc gatggctctt tttagagcat 721
Ser

tttcacttga gctcgtatca tctaggactt tcatttttga ctggattctg ttacactttt 781

cagtaagctg attttgcttt ttttgcagtt caataatttg tgctttgatt tcatctatgt 841

ctaaatcatc gtcacgcgtt aggctga 868

<210> 14
<211> 156
<212> PRT
<213> Bacillus subtilis

<400> 14

Met Val Thr Gly Val Phe Ala Ala Leu Gly Phe Val Val Lys Glu Leu
1 5 10 15

Val Phe Leu Val Ser Tyr Val Lys Asn Asn Ala Phe Pro Gln Pro Leu
20 25 30

Ser Ser Ser Glu Glu Lys Lys Tyr Leu Glu Leu Met Ala Lys Gly Asp
35 40 45

Glu His Ala Arg Asn Met Leu Ile Glu His Asn Leu Arg Leu Val Ala
50 55 60

His Ile Val Lys Lys Phe Glu Asn Thr Gly Glu Asp Ala Glu Asp Leu
65 70 75 80

Ile Ser Ile Gly Thr Ile Gly Leu Ile Lys Gly Ile Glu Ser Tyr Ser
85 90 95

Ala Gly Lys Gly Thr Lys Val Ala Thr Tyr Ala Ala Arg Cys Ile Glu
100 105 110

Asn Glu Ile Val Ile Thr Lys Gly Gly Cys Ile His Pro Ser Leu Ile
115 120 125

Arg Phe Asn Ile Tyr Gly Val Arg Ile His Asn Gly Asn Phe Phe His
130 135 140

H 06291/PCT

Asp Lys Val Asn Asn Cys Phe Phe Ile Phe Lys Ser
145 150 155

<210> 15
<211> 1192
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (201)..(995)
<223>

<220>
<221> gene
<222> (1)..(1192)
<223> spoIVFA

<400> 15
acaaaggaat gatggctaag attaagtcac ttttcggagt aagatcttaa tgtgatagaa 60
tcaaagagaa gaatctgaca aagcatatgc tgtgtcaggt ttttttttgt ttttgcctgc 120
tttgttcttg actaaaccga atatttgcca tggacaagac atatgatgta caaacccaac 180
gaatgcaaag gatgatggca atg agt cac aga gca gat gaa atc aga aaa cga 233
Met Ser His Arg Ala Asp Glu Ile Arg Lys Arg
1 5 10
tta gag aaa aga aga aag cag ctt tcc ggc tca aaa cgt ttc tct act 281
Leu Glu Lys Arg Arg Lys Gln Leu Ser Gly Ser Lys Arg Phe Ser Thr
15 20 25
cag aca gtt tct gaa aag cag aaa ccc ccg tcc tgg gtg atg gta acg 329
Gln Thr Val Ser Glu Lys Gln Lys Pro Pro Ser Trp Val Met Val Thr
30 35 40
gat cag gaa aag cat gga aca ctt ccg gtc tac gaa gat aac atg cca 377
Asp Gln Glu Lys His Gly Thr Leu Pro Val Tyr Glu Asp Asn Met Pro
45 50 55
aca ttc aac gga aaa cac cca ttg gtg aaa aca gat tca att atc ctg 425
Thr Phe Asn Gly Lys His Pro Leu Val Lys Thr Asp Ser Ile Ile Leu
60 65 70 75
aaa tgt ctt ctg tcg gcc tgc ctt gtt ctc gtt tca gct ata gcc tat 473
Lys Cys Leu Leu Ser Ala Cys Leu Val Leu Val Ser Ala Ile Ala Tyr
80 85 90
aaa aca aac att gga ccc gtc agt cag att aaa ccc gcc gta gcc aaa 521
Lys Thr Asn Ile Gly Pro Val Ser Gln Ile Lys Pro Ala Val Ala Lys
95 100 105
acc ttt gaa act gaa ttt caa ttt gct tca gca agc cat tgg ttc gaa 569
Thr Phe Glu Thr Glu Phe Gln Phe Ala Ser Ala Ser His Trp Phe Glu
110 115 120

H 06291/PCT

acc aaa ttc gga aat ccg ctt gct ttc ctg gct cct gaa cac aaa aat 617
 Thr Lys Phe Gly Asn Pro Leu Ala Phe Leu Ala Pro Glu His Lys Asn
 125 130 135

aag gaa cag cag att gaa gta ggc aaa gat ctg atc gcg cct gca tcc 665
 Lys Glu Gln Gln Ile Glu Val Gly Lys Asp Leu Ile Ala Pro Ala Ser
 140 145 150 155

ggg aaa gta cag cag gat ttt cag gac aat ggg gaa gga att aaa gtc 713
 Gly Lys Val Gln Gln Asp Phe Gln Asp Asn Gly Glu Gly Ile Lys Val
 160 165 170

gaa aca agc agt gat aag att gat agc gta aaa gaa ggc tat gtg gtt 761
 Glu Thr Ser Ser Asp Lys Ile Asp Ser Val Lys Glu Gly Tyr Val Val
 175 180 185

gaa gtc agc aaa gac agc caa acg gga ctg acg gtt aag gtg cag cat 809
 Glu Val Ser Lys Asp Ser Gln Thr Gly Leu Thr Val Lys Val Gln His
 190 195 200

gct gac aac acc tat agt atc tat ggc gag ctc aaa gat gtg gat gtt 857
 Ala Asp Asn Thr Tyr Ser Ile Tyr Gly Glu Leu Lys Asp Val Asp Val
 205 210 215

gct tta tat gat ttt gtg gat aaa ggc aaa aag ctc ggt tcg att aag 905
 Ala Leu Tyr Asp Phe Val Asp Lys Gly Lys Lys Leu Gly Ser Ile Lys
 220 225 230 235

ctt gat gat cat aat aaa ggg gtc tat tat ttt gcc atg aaa gac ggc 953
 Leu Asp Asp His Asn Lys Gly Val Tyr Tyr Phe Ala Met Lys Asp Gly
 240 245 250

gat aaa ttt att gat ccg att cag gtg att tca ttt gaa taa 995
 Asp Lys Phe Ile Asp Pro Ile Gln Val Ile Ser Phe Glu
 255 260

atggctcgac cttatcttaa agatccatgt gcaccccttt ctttgattta ttgcggcgct 1055

gggcttgctc acaggccata tgaaagcatt attatgtctg ctcttgattg tattgattca 1115

tgagctgggg catgctgctc tggctgtgtt ttttcttgga agaatacaagc gtgttttttt 1175

gctgccgttt ggcggaa 1192

<210> 16
 <211> 264
 <212> PRT
 <213> Bacillus subtilis

<400> 16

Met Ser His Arg Ala Asp Glu Ile Arg Lys Arg Leu Glu Lys Arg Arg
 1 5 10 15

Lys Gln Leu Ser Gly Ser Lys Arg Phe Ser Thr Gln Thr Val Ser Glu
 20 25 30

H 06291/PCT

Lys Gln Lys Pro Pro Ser Trp Val Met Val Thr Asp Gln Glu Lys His
35 40 45

Gly Thr Leu Pro Val Tyr Glu Asp Asn Met Pro Thr Phe Asn Gly Lys
50 55 60

His Pro Leu Val Lys Thr Asp Ser Ile Ile Leu Lys Cys Leu Leu Ser
65 70 75 80

Ala Cys Leu Val Leu Val Ser Ala Ile Ala Tyr Lys Thr Asn Ile Gly
85 90 95

Pro Val Ser Gln Ile Lys Pro Ala Val Ala Lys Thr Phe Glu Thr Glu
100 105 110

Phe Gln Phe Ala Ser Ala Ser His Trp Phe Glu Thr Lys Phe Gly Asn
115 120 125

Pro Leu Ala Phe Leu Ala Pro Glu His Lys Asn Lys Glu Gln Gln Ile
130 135 140

Glu Val Gly Lys Asp Leu Ile Ala Pro Ala Ser Gly Lys Val Gln Gln
145 150 155 160

Asp Phe Gln Asp Asn Gly Glu Gly Ile Lys Val Glu Thr Ser Ser Asp
165 170 175

Lys Ile Asp Ser Val Lys Glu Gly Tyr Val Val Glu Val Ser Lys Asp
180 185 190

Ser Gln Thr Gly Leu Thr Val Lys Val Gln His Ala Asp Asn Thr Tyr
195 200 205

Ser Ile Tyr Gly Glu Leu Lys Asp Val Asp Val Ala Leu Tyr Asp Phe
210 215 220

Val Asp Lys Gly Lys Lys Leu Gly Ser Ile Lys Leu Asp Asp His Asn
225 230 235 240

Lys Gly Val Tyr Tyr Phe Ala Met Lys Asp Gly Asp Lys Phe Ile Asp
245 250 255

Pro Ile Gln Val Ile Ser Phe Glu
260

<210> 17

H 06291/PCT

<211> 1264
<212> DNA
<213> Bacillus subtilis

<220>
<221> CDS
<222> (201)..(1067)
<223>

<220>
<221> gene
<222> (1)..(1264)
<223> spoIVFB

<220>
<221> misc_feature
<222> (201)..(203)
<223> First codon translated as Met.

<400> 17
actgacgggtt aaggtgcagc atgctgacaa cacctatagt atctatggcg agctcaaaga 60
tgtggatggtt gctttatatg attttgtgga taaaggcaaa aagctcgggtt cgattaagct 120
tgatgatcat aataaagggg tctattatatt tgccatgaaa gacggcgata aatttattga 180
tccgattcag gtgatttcat ttg aat aaa tgg ctc gac ctt atc tta aag atc 233
Leu Asn Lys Trp Leu Asp Leu Ile Leu Lys Ile
1 5 10
cat gtg cat cct ttt ctt tgg att att gcg gcg ctg ggc ttg ctc aca 281
His Val His Pro Phe Leu Trp Ile Ile Ala Ala Leu Gly Leu Leu Thr
15 20 25
ggc cat atg aaa gca tta tta tgt ctg ctc ctg att gta ttg att cat 329
Gly His Met Lys Ala Leu Leu Cys Leu Leu Leu Ile Val Leu Ile His
30 35 40
gag ctg ggg cat gct gct ctg gct gtg ttt ttt tct tgg aga atc aag 377
Glu Leu Gly His Ala Ala Leu Ala Val Phe Phe Ser Trp Arg Ile Lys
45 50 55
cgt gtt ttt ttg ctg ccg ttt ggc gga acg gtc gaa gtg gaa gag cac 425
Arg Val Phe Leu Leu Pro Phe Gly Gly Thr Val Glu Val Glu Glu His
60 65 70 75
ggg aat cgg ccg tta aag gaa gag ttt gcg gtc att att gcc gga cct 473
Gly Asn Arg Pro Leu Lys Glu Glu Phe Ala Val Ile Ile Ala Gly Pro
80 85 90
ctt cag cac atc tgg ctt cag ttt gcc gcc tgg atg ctt gca gaa gtc 521
Leu Gln His Ile Trp Leu Gln Phe Ala Ala Trp Met Leu Ala Glu Val
95 100 105
tca gtg att cat cag cat acc ttt gaa ctc ttc acc ttt tat aat ctt 569
Ser Val Ile His Gln His Thr Phe Glu Leu Phe Thr Phe Tyr Asn Leu
110 115 120

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tct atc tta ttt gtc aat tta ctg ccg atc tgg ccg ctg gat gga gga	617
Ser Ile Leu Phe Val Asn Leu Leu Pro Ile Trp Pro Leu Asp Gly Gly	
125 130 135	
aaa ctg tta ttt ttg ttg ttt tcc aaa cag ctg cct ttt caa aag gct	665
Lys Leu Leu Phe Leu Leu Phe Ser Lys Gln Leu Pro Phe Gln Lys Ala	
140 145 150 155	
cac cgg ctt aat cta aaa acg tcg ctc tgc ttc tgc ctg ctg ctc ggg	713
His Arg Leu Asn Leu Lys Thr Ser Leu Cys Phe Cys Leu Leu Leu Gly	
160 165 170	
tgc tgg gtt tta ttc gtg att cct ctg caa atc agc gca tgg gtt ttg	761
Cys Trp Val Leu Phe Val Ile Pro Leu Gln Ile Ser Ala Trp Val Leu	
175 180 185	
ttt gtc ttt ctg gct gtt tcc ttg ttt gag gaa tat cgg caa agg cac	809
Phe Val Phe Leu Ala Val Ser Leu Phe Glu Glu Tyr Arg Gln Arg His	
190 195 200	
tat atc cat gtg aga ttt ctc ctc gaa agg tat tac gga aaa aac agg	857
Tyr Ile His Val Arg Phe Leu Leu Glu Arg Tyr Tyr Gly Lys Asn Arg	
205 210 215	
gag ctt gag aaa ctt ctg ccg ctg aca gta aag gcg gag gat aaa gtc	905
Glu Leu Glu Lys Leu Leu Pro Leu Thr Val Lys Ala Glu Asp Lys Val	
220 225 230 235	
tat cat gtg atg gcc gag ttc aaa cgt ggc tgt aag cat ccg att att	953
Tyr His Val Met Ala Glu Phe Lys Arg Gly Cys Lys His Pro Ile Ile	
240 245 250	
ata gaa aaa tca ggc caa aag ctc agc cag ctt gac gag aat gaa gtg	1001
Ile Glu Lys Ser Gly Gln Lys Leu Ser Gln Leu Asp Glu Asn Glu Val	
255 260 265	
ctg cac gct tac ttt gcc gat aag cgg acg aat tct tcc atg gag gaa	1049
Leu His Ala Tyr Phe Ala Asp Lys Arg Thr Asn Ser Ser Met Glu Glu	
270 275 280	
ctg ctt ctg ccc tac taa aactgattga caaacgcctt gtattttggt	1097
Leu Leu Leu Pro Tyr	
285	
atatttttta atgttatgga tgtagcacca ttgctacaac cgctcagtac aggtgttaag	1157
agctttttaca gccccctggt atctggcgag tcttagtcta ataggaggtg cagagaatgt	1217
acgcaatcat taaaacaggc ggtaaacaaa tcaaagttga agaaggc	1264

<210> 18
 <211> 288
 <212> PRT
 <213> Bacillus subtilis

<220>
 <221> misc_feature
 <222> (201)..(203)
 <223> First codon translated as Met.

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<400> 18

Leu Asn Lys Trp Leu Asp Leu Ile Leu Lys Ile His Val His Pro Phe
1 5 10 15

Leu Trp Ile Ile Ala Ala Leu Gly Leu Leu Thr Gly His Met Lys Ala
20 25 30

Leu Leu Cys Leu Leu Leu Ile Val Leu Ile His Glu Leu Gly His Ala
35 40 45

Ala Leu Ala Val Phe Phe Ser Trp Arg Ile Lys Arg Val Phe Leu Leu
50 55 60

Pro Phe Gly Gly Thr Val Glu Val Glu Glu His Gly Asn Arg Pro Leu
65 70 75 80

Lys Glu Glu Phe Ala Val Ile Ile Ala Gly Pro Leu Gln His Ile Trp
85 90 95

Leu Gln Phe Ala Ala Trp Met Leu Ala Glu Val Ser Val Ile His Gln
100 105 110

His Thr Phe Glu Leu Phe Thr Phe Tyr Asn Leu Ser Ile Leu Phe Val
115 120 125

Asn Leu Leu Pro Ile Trp Pro Leu Asp Gly Gly Lys Leu Leu Phe Leu
130 135 140

Leu Phe Ser Lys Gln Leu Pro Phe Gln Lys Ala His Arg Leu Asn Leu
145 150 155 160

Lys Thr Ser Leu Cys Phe Cys Leu Leu Leu Gly Cys Trp Val Leu Phe
165 170 175

Val Ile Pro Leu Gln Ile Ser Ala Trp Val Leu Phe Val Phe Leu Ala
180 185 190

Val Ser Leu Phe Glu Glu Tyr Arg Gln Arg His Tyr Ile His Val Arg
195 200 205

Phe Leu Leu Glu Arg Tyr Tyr Gly Lys Asn Arg Glu Leu Glu Lys Leu
210 215 220

Leu Pro Leu Thr Val Lys Ala Glu Asp Lys Val Tyr His Val Met Ala
225 230 235 240

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Glu Phe Lys Arg Gly Cys Lys His Pro Ile Ile Ile Glu Lys Ser Gly
245 250 255

Gln Lys Leu Ser Gln Leu Asp Glu Asn Glu Val Leu His Ala Tyr Phe
260 265 270

Ala Asp Lys Arg Thr Asn Ser Ser Met Glu Glu Leu Leu Leu Pro Tyr
275 280 285

<210> 19
<211> 29
<212> DNA
<213> Artificial sequence

<220>
<223> PCR-Primer spo1

<400> 19
ggctgatgct caaacagggg cagtgcac 29

<210> 20
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR-Primer spo2

<400> 20
catgaacggc ctttacgaca gcca 24

<210> 21
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR-Primer spo3

<400> 21
gtcatcaaaa cgattttgcc tgagg 25

<210> 22
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR-Primer spo4

<400> 22
atgttctgtc ccgggattgg ctctg 26

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<210> 23
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR-Primer spo6

<400> 23
gttttgactc tgatcggaat tctttggcg

29

<210> 24
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR-Primer spo7

<400> 24
gcacgaaacg agcgagaatg gc

22

<210> 25
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR-Primer recA1

<400> 25
ggaattcggc atcagcttca ctggag

26

<210> 26
<211> 29
<212> DNA
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<220>
<223> PCR-Primer recA2

<400> 26
gctatgtcga ctataccttg tttatgcgg

29

<210> 27
<211> 21
<212> DNA
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<220>
<223> PCR-Primer recA3

<400> 27
gacctcgga cagagcttga c

21

<210> 28

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<211> 30
<212> DNA
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<220>
<223> PCR-Primer recA4

<400> 28
tcaaaactgca gtcattaaga gaatggatgg 30

<210> 29
<211> 23
<212> DNA
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<220>
<223> PCR-Primer recA5

<400> 29
aagcttacgg tttaacgttt ctg 23

<210> 30
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR-Primer recA6

<400> 30
acacaaacga attgaaagtg tcagcg 26

<210> 31
<211> 1557
<212> DNA
<213> Bacillus licheniformis A

<220>
<221> CDS
<222> (369)..(1415)
<223>

<220>
<221> gene
<222> (1)..(1557)
<223> recA

<400> 31
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ggaaaggtgt ttatcgcat ctccgtgaag gaccaggctg aggaagcggt cgaatttcag 120
ttcgccggat ccaggtctgc ggtgcggaag cgttctgcc aatacggctg ccatctgttg 180
ctgaaaatga tggaaaaata agcggaaacc ggattttcgg aatatctttc tttcgaaaaa 240

H 06291/PCT

gccattcca ttttaggaga tcgatttttc ctcttaaaaa aatcgaatat gcgttcgctt 300
 ttttcttggc aaatccgcat aaacaaggta tagtagatat agcggaagtg ataaaggagg 360
 aaaataga atg agt gat cgt cag gca gcc tta gat atg gcg ctt aaa caa 410
 Met Ser Asp Arg Gln Ala Ala Leu Asp Met Ala Leu Lys Gln
 1 5 10
 ata gaa aag cag ttt ggt aaa ggt tcg att atg aaa ctc ggc gaa caa 458
 Ile Glu Lys Gln Phe Gly Lys Gly Ser Ile Met Lys Leu Gly Glu Gln
 15 20 25 30
 act gaa acg aga att tca aca gtt ccg agc ggt tct tta gcg ctc gat 506
 Thr Glu Thr Arg Ile Ser Thr Val Pro Ser Gly Ser Leu Ala Leu Asp
 35 40 45
 gcg gct ctt gga gtg ggc gga tac ccg cgc ggc cgg att att gaa gta 554
 Ala Ala Leu Gly Val Gly Gly Tyr Pro Arg Gly Arg Ile Ile Glu Val
 50 55 60
 tac ggg cct gaa agc tcc ggt aaa acg acg gtg gcg ctt cat gcg att 602
 Tyr Gly Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile
 65 70 75
 gcc gaa gtt cag cag cag ggc gga caa gcg gcg ttc atc gac gcc gaa 650
 Ala Glu Val Gln Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Glu
 80 85 90
 cac gcg ctt gat ccc gtc tat gca caa aag ctg ggc gtc aac att gat 698
 His Ala Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp
 95 100 105 110
 gag ctt ttg ctg tca cag cct gat acg ggc gag cag gcg ctc gaa atc 746
 Glu Leu Leu Leu Ser Gln Pro Asp Thr Gly Glu Gln Ala Leu Glu Ile
 115 120 125
 gct gaa gcc ctt gtc aga agc gga gcg gtg gat atc gtt gtc atc gac 794
 Ala Glu Ala Leu Val Arg Ser Gly Ala Val Asp Ile Val Val Ile Asp
 130 135 140
 tct gta gca gcg ctt gtg ccg aaa gct gaa atc gaa gga gat atg ggg 842
 Ser Val Ala Ala Leu Val Pro Lys Ala Glu Ile Glu Gly Asp Met Gly
 145 150 155
 gat tcc cac gtc ggt ttg cag gcc aga ctg atg tct cag gcg ctt cgc 890
 Asp Ser His Val Gly Leu Gln Ala Arg Leu Met Ser Gln Ala Leu Arg
 160 165 170
 aag ctt tcc gga gcg atc aat aaa tcg aag acc atc gcg atc ttt atc 938
 Lys Leu Ser Gly Ala Ile Asn Lys Ser Lys Thr Ile Ala Ile Phe Ile
 175 180 185 190
 aac cag att cgt gaa aaa gtc ggt gtc atg ttt gga aat cct gag acg 986
 Asn Gln Ile Arg Glu Lys Val Gly Val Met Phe Gly Asn Pro Glu Thr
 195 200 205
 acg cca ggc gga aga gcg ctg aaa ttc tac tct tct gtc cgc ctt gaa 1034
 Thr Pro Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Val Arg Leu Glu
 210 215 220
 gtg cgc cgc gca gag cag ctg aaa caa ggc aac gac gtc atg ggg aac 1082

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Val	Arg	Arg	Ala	Glu	Gln	Leu	Lys	Gln	Gly	Asn	Asp	Val	Met	Gly	Asn		
		225					230					235					
aag	acg	aaa	atc	aaa	gtc	gtg	aaa	aac	aaa	gtg	gca	cct	cca	ttc	cgg	1130	
Lys	Thr	Lys	Ile	Lys	Val	Val	Lys	Asn	Lys	Val	Ala	Pro	Pro	Phe	Arg		
	240					245					250						
aca	gcc	gaa	gtg	gac	att	atg	tac	ggg	gaa	gga	att	tca	aaa	gaa	ggg	1178	
Thr	Ala	Glu	Val	Asp	Ile	Met	Tyr	Gly	Glu	Gly	Ile	Ser	Lys	Glu	Gly		
255					260					265					270		
gaa	atc	atc	gac	ctc	gga	aca	gag	ctt	gac	atc	gtt	caa	aag	agc	ggg	1226	
Glu	Ile	Ile	Asp	Leu	Gly	Thr	Glu	Leu	Asp	Ile	Val	Gln	Lys	Ser	Gly		
				275					280					285			
gca	tgg	tac	tct	tat	cag	gag	gaa	cgc	ctt	gga	caa	ggc	cgt	gaa	aac	1274	
Ala	Trp	Tyr	Ser	Tyr	Gln	Glu	Glu	Arg	Leu	Gly	Gln	Gly	Arg	Glu	Asn		
			290					295					300				
gcc	aaa	cag	ttc	ctg	aaa	gaa	aac	aag	gat	atc	ctt	ttg	atg	att	caa	1322	
Ala	Lys	Gln	Phe	Leu	Lys	Glu	Asn	Lys	Asp	Ile	Leu	Leu	Met	Ile	Gln		
		305					310					315					
gag	cag	atc	cgg	gag	cac	tac	ggg	ttg	gat	act	gga	ggc	gct	gct	cct	1370	
Glu	Gln	Ile	Arg	Glu	His	Tyr	Gly	Leu	Asp	Thr	Gly	Gly	Ala	Ala	Pro		
	320					325					330						
gca	cag	gaa	gac	gag	gcc	caa	gct	cag	gaa	gaa	ctc	gag	ttt	taa		1415	
Ala	Gln	Glu	Asp	Glu	Ala	Gln	Ala	Gln	Glu	Glu	Leu	Glu	Phe				
335					340					345							
tcatgaaacg tgtgaaaggc tgccggcccg atcggcagcc ttttacttta ttcttcgctt																	1475
tcaggcgctt ctcttccatc cattctctta atgagggcag tttgaaaggc gtttaatcca																	1535
gaaacgtaa gaccgtaagc tt																	1557

<210> 32
 <211> 348
 <212> PRT
 <213> Bacillus licheniformis A

<400> 32

Met	Ser	Asp	Arg	Gln	Ala	Ala	Leu	Asp	Met	Ala	Leu	Lys	Gln	Ile	Glu		
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Lys	Gln	Phe	Gly	Lys	Gly	Ser	Ile	Met	Lys	Leu	Gly	Glu	Gln	Thr	Glu		
		20						25					30				
Thr	Arg	Ile	Ser	Thr	Val	Pro	Ser	Gly	Ser	Leu	Ala	Leu	Asp	Ala	Ala		
	35						40					45					
Leu	Gly	Val	Gly	Gly	Tyr	Pro	Arg	Gly	Arg	Ile	Ile	Glu	Val	Tyr	Gly		
	50					55					60						

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Pro Glu Ser Ser Gly Lys Thr Thr Val Ala Leu His Ala Ile Ala Glu
65 70 75 80

Val Gln Gln Gln Gly Gly Gln Ala Ala Phe Ile Asp Ala Glu His Ala
85 90 95

Leu Asp Pro Val Tyr Ala Gln Lys Leu Gly Val Asn Ile Asp Glu Leu
100 105 110

Leu Leu Ser Gln Pro Asp Thr Gly Glu Gln Ala Leu Glu Ile Ala Glu
115 120 125

Ala Leu Val Arg Ser Gly Ala Val Asp Ile Val Val Ile Asp Ser Val
130 135 140

Ala Ala Leu Val Pro Lys Ala Glu Ile Glu Gly Asp Met Gly Asp Ser
145 150 155 160

His Val Gly Leu Gln Ala Arg Leu Met Ser Gln Ala Leu Arg Lys Leu
165 170 175

Ser Gly Ala Ile Asn Lys Ser Lys Thr Ile Ala Ile Phe Ile Asn Gln
180 185 190

Ile Arg Glu Lys Val Gly Val Met Phe Gly Asn Pro Glu Thr Thr Pro
195 200 205

Gly Gly Arg Ala Leu Lys Phe Tyr Ser Ser Val Arg Leu Glu Val Arg
210 215 220

Arg Ala Glu Gln Leu Lys Gln Gly Asn Asp Val Met Gly Asn Lys Thr
225 230 235 240

Lys Ile Lys Val Val Lys Asn Lys Val Ala Pro Pro Phe Arg Thr Ala
245 250 255

Glu Val Asp Ile Met Tyr Gly Glu Gly Ile Ser Lys Glu Gly Glu Ile
260 265 270

Ile Asp Leu Gly Thr Glu Leu Asp Ile Val Gln Lys Ser Gly Ala Trp
275 280 285

Tyr Ser Tyr Gln Glu Glu Arg Leu Gly Gln Gly Arg Glu Asn Ala Lys
290 295 300

Gln Phe Leu Lys Glu Asn Lys Asp Ile Leu Leu Met Ile Gln Glu Gln

305 310 315 320

Ile Arg Glu His Tyr Gly Leu Asp Thr Gly Gly Ala Ala Pro Ala Gln
325 330 335

Glu Asp Glu Ala Gln Ala Gln Glu Glu Leu Glu Phe
340 345